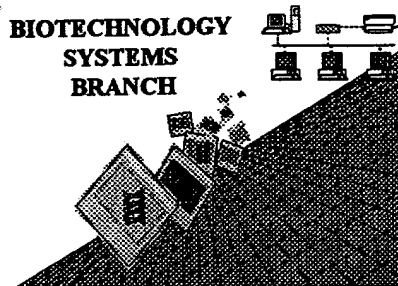


R. Landsman.

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/431,843A (RustH)

Art Unit / Team No. : 1646

Date Processed by STIC: 4/19/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/431,843A

DATE: 04/19/2000
TIME: 09:30:57

Input Set: I431843A.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

1 <110> Zagon S., Ian
2 Verderame, Michael
3 Allen, Sandra
4 McLaughlin J., Patricia
5 <120> NOVEL NUCLEIC ACID MOLECULES ENCODING OPIOID GROWTH
6 FACTOR RECEPTORS
7 <130> Penn State
8 <140> US/09/431,843A
9 <141> 1999-11-02
10 <160> 18
11 <170> PatentIn Ver. 2.1.

Does Not Comply
Corrected Diskette Needed

see page 3-4
for more
errors

ERRORED SEQUENCES FOLLOW

E--> 12 <210> 8
13 <211> 461
14 <212> PRT
15 <213> Homo sapiens
16 <400> 8
17 Met Asp Asp Pro Asp Cys Asp Ser Thr Trp Glu Glu Asp Glu Glu Asp
18 1 5 10 15
19 Ala Glu Asp Ala Glu Asp Glu Asp Cys Glu Asp Gly Glu Ala Ala Gly
20 20 25 30
21 Ala Arg Asp Ala Asp Ala Gly Asp Glu Asp Glu Glu Ser Glu Glu Pro
22 35 40 45
23 Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Leu Thr Gly Ser
24 50 55 60
25 Arg Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr
26 65 70 75 80
27 Pro Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser
28 85 90 95
29 Phe Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu
30 100 105 110
31 Asp Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn
32 115 120 125
33 His Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn
34 130 135 140
35 Trp His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser
36 145 150 155 160
37 Ser Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu
38 165 170 175
39 Gly Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly

← sequence has 462

remove
Leu

PAGE: 2

RAW SEQUENCE LISTING
 PATENT APPLICATION US/09/431,843A

DATE: 04/19/2000
 TIME: 09:30:57

Input Set: I431843A.RAW

40		180		185		190	
41	Arg	Ala	Gln	Asn	Tyr	Gln	Lys
42		195		200		205	
43	His	Asn	Asn	Leu	Arg	Ile	Thr
44		210		215		220	
45	Ser	Leu	Glu	His	Phe	Gln	Ala
46		225		230		235	
47	Thr	Leu	Val	Arg	Arg	Glu	Leu
48			245			250	
49	Tyr	Phe	Met	Phe	Ala	Val	Arg
50			260			265	
51	His	Phe	Ala	Trp	Glu	His	Phe
52			275			280	
53	Pro	Gln	Asp	Lys	Leu	Arg	Arg
54			290			295	
55	Leu	Glu	Gly	Ser	Arg	Lys	Val
56			305			310	
57	Asp	His	Glu	Ala	Ser	Thr	Gln
58				325			330
59	Lys	Gly	Gly	Gly	Arg	Val	Asp
60				340			345
61	Pro	Gln	Asp	Ala	Gly	Pro	Leu
62			355			360	
63	Gly	His	Gly	Glu	Asp	Arg	Pro
64			370			375	
65	Lys	Arg	Lys	Leu	Glu	Leu	Ser
66				385		390	
67	Gly	Pro	Gln	Ser	Ala	Ser	Glu
68				405			410
69	Gly	Cys	Ala	Leu	Ser	Gln	Gly
70				420			425
71	Gly	Gly	Gln	Asp	Pro	Gly	Glu
72			435			440	
73	Gly	Leu	Arg	Ser	Cys	Cys	Gly
74			450			455	

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/43/843A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 **Misaligned Amino Acid
Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 **Variable Length** Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 **Use of <213>Organism
(NEW RULES)** Sequence(s) are missing this mandatory field or its response.
- 12 **Use of <220>Feature
(NEW RULES)** Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 **PatentIn ver. 2.0 "bug"** **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.